

**(1) GENERAL INFORMATION:**

- (i) APPLICANTS: Seed, Brian et al.
- (ii) TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor Chimeras
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson
  - (B) STREET: 225 Franklin Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
  - (B) COMPUTER: IBM PS/2 Model 50Z or 55SX
  - (C) OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
  - (D) SOFTWARE: Wordperfect (Version 5.0)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/203,866
  - (B) FILING DATE: February 28, 1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/847,566
  - (B) FILING DATE: March 6, 1992
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/665,961
  - (B) FILING DATE: March 7, 1991
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Clark, Paul T.
  - (B) REGISTRATION NUMBER: 30,162
  - (C) REFERENCE/DOCKET NUMBER: 00786/270001
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 542-5070
  - (B) TELEFAX: (617) 542-8906
  - (C) TELEX: 200154

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1728 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	TGCAACTGGC	50
GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	GGCAAAAAG	100
GGGATACAGT	GGAAGTGACC	TGTACAGCTT	CCCAGAAGAA	GAGCATACAA	150
TTCCACTGGA	AAAAGTCCAA	CCAGATAAAG	ATTCTGGGAA	ATCAGGGCTC	200
CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	GACTCAAGAA	250
GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	GAATCTTAAG	300
ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	AGAAGGAGGA	350
GGTGCAATTG	CTAGTGTTTG	GATTGACTGC	CAACTCTGAC	ACCCACCTGC	400
TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	TGGTAGTAGC	450
CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	AGGGGGGGAA	500
GACCCCTCTC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	ACCTGGACAT	550
GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	AGACATCGTG	600
GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	AAGAGGGGGA	650
ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	AAGCTGACGG	700
GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	CTCCAAGTCT	750
TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	AACGGGTTAC	800
CCAGGACCCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	CACCTCACCC	850
TGCCCCAGGC	CTTGCCCTCAG	TATGCTGGCT	CTGGAAACCT	CACCCTGGCC	900
CTTGAAGCGA	AAACAGGAAA	GTTGCATCAG	GAAGTGAACC	TGGTGGTGAT	950
GAGAGCCACT	CAGCTCCAGA	AAAATTTGAC	CTGTGAGGTG	TGGGGACCCA	1000
CCTCCCCCTAA	GCTGATGCTG	AGCTTGAAAC	TGGAGAACAA	GGAGGCAAAG	1050
GTCTCGAAGC	GGGAGAAGCC	GGTGTGGGTG	CTGAACCCTG	AGGCGGGGAT	1100
GTGGCAGTGT	CTGCTGAGTG	ACTCGGGACA	GGTCCTGCTG	GAATCCAACA	1150
<hr/>					
TCAAGGTTCT	GCCCACATGG	TCCACCCCGG	TGCACGCGGA	TCCCAAATC	1200
TGCTACTTGC	TAGATGGAAT	CCTCTTCATC	TACGGAGTCA	TCATCACAGC	1250
CCTGTACCTG	AGAGCAAAAT	TCAGCAGGAG	TGCAGAGACT	GCTGCCAACC	1300
TGCAGGACCC	CAACCAGCTC	TACAATGAGC	TCAATCTAGG	GCGAAGAGA	1350
GAATATGACG	TCTTGGAGAA	GAAGCGGGCT	CGGGATCCAG	AGATGGGAGG	1400

09243008.020299

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 1389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	TGCAAACTGGC	50
GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	GGCAAAAAAG	100
GGGATACAGT	GGAACTGACC	TGTACAGCTT	CCCAGAAGAA	GAGCATACAA	150
TTCCACTGGA	AAAAC TCCAA	CCAGATAAAG	ATTCTGGGAA	ATCAGGGCTC	200
CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	GACTCAAGAA	250
GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	GAATCTTAAG	300
ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	AGAAGGAGGA	350
GGTGCAATTG	CTAGTGTTCTG	GATTGACTGC	CAACTCTGAC	ACCCACCTGC	400
TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	TGGTAGTAGC	450
CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	AGGGGGGGAA	500
GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	ACCTGGACAT	550
GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	AGACATCGTG	600
GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	AAGAGGGGGA	650
ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	AAGCTGACGG	700
GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	CTCCAAGTCT	750
TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	AACGGGTTAC	800
CCAGGACCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	CACCTCACCC	850

TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCATCA GAAGTGAACC TGGTGGTGAT	950
GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGGCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTGCTG GAATCCAACA	1150
TCAAGGTTCT GCCACATGG TCCACCCCGG TGCACGCGGA TCCGCAGCTC	1200
TGCTATATCC TGGATGCCAT CCTGTTTTTG TATGGTATTG TCCTTACCCT	1250
GCTCTACTGT CGACTCAAGA TCCAGGTCCG AAAGGCAGAC ATAGCCAGCC	1300
GTGAGAAATC AGATGCTGTC TACACGGGCC TGAACACCCG GAACCAGGAG	1350
ACATATGAGA CTCTGAAACA TGAGAAACCA CCCCAATAG	1389

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG	100
GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA GAGCATACAA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTTC GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAACATAC AGGGGGGGAA	500
GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650

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ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750
TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC TGGTGGTGAT	950
GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGGCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTGCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA TCCCAAATC	1200
TGCTACCTGC TGGATGGAAT CCTCTTCATC TATGGTGTCA TTCTCACTGC	1250
CTTGTTCTCTG AGAGTGAAGT TCAGCAGGAG CGCAGAGCCC CCCGCGTACC	1300
AGCAGGGCCA GAACCAGCTC TATAACGAGC TCAATCTAGG ACGAAGAGAG	1350
GAGTACGATG TTTTGGACAA GAGACGTGGC CGGGACCCTG AGATGGGGGG	1400
AAAGCCGAGA AGGAAGAACC CTCAGGAAGG CCTGTACAAT GAACTGCAGA	1450
AAGATAAGAT GGCGGAGGCC TACAGTGAGA TTGGGATGAA AGGCGAGCGC	1500
CGGAGGGGCA AGGGGCACGA TGGCCTTTAC CAGGGTCTCA GTACAGCCAC	1550
CAAGGACACC TACGACGCCC TTCACATGCA GGCCCTGCCC CCTCGCTAA	1599

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Val	Leu	Gln	Leu
1				5					10				15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly
			20					25					30	Lys
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys
		35					40				45			Ser
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly
	50				55					60				Asn
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg
	65				70				75					80
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	L u	Ile
			85					90					95	Ile

Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
100								105					110		
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
115							120					125			
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
130						135					140				
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
145					150					155					160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
165									170					175	
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
180								185					190		
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
195							200					205			
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
210						215					220				
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
225					230					235					240
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
245									250					255	
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
260								265					270		
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
275							280					285			
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
290						295					300				
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
305					310					315					320
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
325									330					335	
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
340								345					350		
Lys	Arg	Glu	Lys	Pro	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
355							360					365			
Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	Glu	Ser	Asn	Ile
370						375					380				
Lys	Val	Leu	Pro	Thr	Trp	Ser	Thr	Pro	Val	His	Ala	Asp	Pro	Lys	Leu
385					390					395					400
Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	Ile	Ile	Thr
405									410					415	
Ala	Leu	Tyr	Leu	Arg	Ala	Lys	Phe	Ser	Arg	Ser	Ala	Glu	Thr	Ala	Ala
420							425						430		
Asn	Leu	Gln	Asp	Pro	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
435							440					445			
Arg	Glu														

**(i) SEQUENCE CHARACTERISTICS:**

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met 1	Asn	Arg	Gly	Val 5	Pro	Phe	Arg	His	Leu 10	Leu	Leu	Val	Leu	Gln 15	Leu
Ala	Leu	Leu	Pro 20	Ala	Ala	Thr	Gln	Gly 25	Asn	Lys	Val	Val	Leu 30	Gly	Lys
Lys	Gly	Asp 35	Thr	Val	Glu	Leu	Thr 40	Cys	Thr	Ala	Ser	Gln 45	Lys	Lys	Ser
Ile	Gln 50	Phe	His	Trp	Lys	Asn 55	Ser	Asn	Gln	Ile	Lys 60	Ile	Leu	Gly	Asn
Gln 65	Gly	Ser	Phe	Leu	Thr 70	Lys	Gly	Pro	Ser	Lys 75	Leu	Asn	Asp	Arg	Ala
Asp	Ser	Arg	Arg	Ser 85	Leu	Trp	Asp	Gln	Gly 90	Asn	Phe	Pro	Leu	Ile 95	Ile
Lys	Asn	Leu	Lys 100	Ile	Glu	Asp	Ser	Asp 105	Thr	Tyr	Ile	Cys	Glu 110	Val	Glu
Asp	Gln 115	Lys	Glu	Glu	Val	Gln	Leu 120	Leu	Val	Phe	Gly	Leu 125	Thr	Ala	Asn
Ser	Asp 130	Thr	His	Leu	Leu	Gln 135	Gly	Gln	Ser	Leu	Thr 140	Leu	Thr	Leu	Glu
Ser 145	Pro	Pro	Gly	Ser	Ser 150	Pro	Ser	Val	Gln	Cys 155	Arg	Ser	Pro	Arg	Gly
Lys	Asn	Ile	Gln 165	Gly	Gly	Lys	Thr	Leu	Ser 170	Val	Ser	Gln	Leu	Glu 175	Leu
Gln	Asp 180	Ser	Gly	Thr	Trp	Thr	Cys 185	Thr	Val	Leu	Gln	Asn 190	Gln	Lys	Lys
Val	Glu 195	Phe	Lys	Ile	Asp	Ile	Val 200	Val	Leu	Ala	Phe	Gln 205	Lys	Ala	Ser
Ser 210	Ile	Val	Tyr	Lys	Lys	Glu 215	Gly	Glu	Gln	Val	Glu 220	Phe	Ser	Phe	Pro
Leu 225	Ala	Phe	Thr	Val	Glu	Lys 230	Leu	Thr	Gly	Ser 235	Gly	Glu	Leu	Trp	Trp
Gln	Ala	Glu	Arg 245	Ala	Ser	Ser	Ser	Lys	Ser 250	Trp	Ile	Thr	Phe	Asp 255	Leu
Lys	Asn	Lys 260	Glu	Val	Ser	Val	Lys	Arg 265	Val	Thr	Gln	Asp 270	Pro	Lys	Leu
Gln	Met 275	Gly	Lys	Lys	Leu	Pro	Leu 280	His	Leu	Thr	Leu 285	Pro	Gln	Ala	Leu
Pro	Gln 290	Tyr	Ala	Gly	Ser	Gly 295	Asn	Leu	Thr	Leu 300	Ala	Leu	Glu	Ala	Lys
Thr 305	Gly	Lys	Leu	His 310	Gln	Glu	Val	Asn	Leu	Val 315	Val	Met	Arg	Ala	Thr
Gln	Leu	Gln	Lys 325	Asn	Leu	Thr	Cys	Glu	Val 330	Trp	Gly	Pro	Thr	Ser 335	Pro
Lys	Leu	Met 340	Leu	Ser	Leu	Lys	Leu 345	Glu	Asn	Lys	Glu	Ala 350	Lys	Val	Ser
Lys	Arg 355	Glu	Lys	Pro	Val	Trp	Val 360	Leu	Asn	Pro	Glu	Ala 365	Gly	Met	Trp
Gln	Cys 370	Leu	Leu	Ser	Asp	Ser 375	Gly	Gln	Val	Leu	Leu 380	Glu	Ser	Asn	Ile
Lys 385	Val	Leu	Pro	Thr	Trp 390	Ser	Thr	Pr	Val	His 395	Ala	Asp	Pro	Gln	Leu
Cys	Tyr	Ile	Leu	Asp	Ala	Ile	Leu	Phe	Leu	Tyr	Gly	Ile	Val	Leu	Thr

**(2) INFORMATION FOR SEQ ID NO:6:**

(A) LENGTH: 532 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met 1	Asn	Arg	Gly	Val 5	Pro	Phe	Arg	His	Leu 10	Leu	Leu	Val	Leu	Gln 15	Leu
Ala	Leu	Leu	Pro 20	Ala	Ala	Thr	Gln	Gly 25	Asn	Lys	Val	Val	Leu	Gly 30	Lys
Lys	Gly	Asp 35	Thr	Val	Glu	Leu	Thr 40	Cys	Thr	Ala	Ser	Gln 45	Lys	Lys	Ser
Ile	Gln 50	Phe	His	Trp	Lys	Asn 55	Ser	Asn	Gln	Ile	Lys 60	Ile	Leu	Gly	Asn
Gln 65	Gly	Ser	Phe	Leu	Thr 70	Lys	Gly	Pro	Ser	Lys 75	Leu	Asn	Asp	Arg	Ala 80
Asp	Ser	Arg	Arg	Ser 85	Leu	Trp	Asp	Gln	Gly 90	Asn	Phe	Pro	Leu	Ile 95	Ile
Lys	Asn	Leu	Lys 100	Ile	Glu	Asp	Ser	Asp 105	Thr	Tyr	Ile	Cys	Glu 110	Val	Glu
Asp	Gln 115	Lys	Glu	Glu	Val	Gln	Leu 120	Leu	Val	Phe	Gly	Leu 125	Thr	Ala	Asn
Ser	Asp 130	Thr	His	Leu	Leu	Gln 135	Gly	Gln	Ser	Leu	Thr 140	Leu	Thr	Leu	Glu
Ser 145	Pro	Pro	Gly	Ser	Ser 150	Pro	Ser	Val	Gln	Cys 155	Arg	Ser	Pro	Arg	Gly 160
Lys	Asn	Ile	Gln 165	Gly	Gly	Lys	Thr	Leu	Ser 170	Val	Ser	Gln	Leu 175	Glu	Leu
Gln	Asp	Ser	Gly 180	Thr	Trp	Thr	Cys	Thr 185	Val	Leu	Gln	Asn	Gln 190	Lys	Lys
Val	Glu 195	Phe	Lys	Ile	Asp	Ile	Val 200	Val	Leu	Ala	Phe	Gln 205	Lys	Ala	Ser
Ser 210	Ile	Val	Tyr	Lys	Lys	Glu 215	Gly	Glu	Gln	Val	Glu 220	Phe	Ser	Phe	Pro
Leu 225	Ala	Phe	Thr	Val	Glu 230	Lys	Leu	Thr	Gly	Ser 235	Gly	Glu	Leu	Trp	Trp 240
Gln	Ala	Glu	Arg 245	Ala	Ser	Ser	Ser	Lys	Ser 250	Trp	Ile	Thr	Phe	Asp 255	Leu
Lys	Asn	Lys	Glu 260	Val	Ser	Val	Lys	Arg 265	Val	Thr	Gln	Asp 270	Pro	Lys	Leu
Gln	Met 275	Gly	Lys	Lys	Leu	Pro	Leu 280	His	Leu	Thr	Leu	Pro 285	Gln	Ala	Leu
Pro	Gln 290	Tyr	Ala	Gly	Ser	Gly 295	Asn	Leu	Thr	Leu	Ala 300	Leu	Glu	Ala	Lys
Thr 305	Gly	Lys	Leu	His	Gln 310	Glu	Val	Asn	Leu	Val 315	Val	Met	Arg	Ala	Thr 320
Gln	Leu	Gln	Lys	Asn 325	Leu	Thr	Cys	Glu	Val 330	Trp	Gly	Pro	Thr	Ser 335	Pro



Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
			340					345					350		
Lys	Arg	Glu	Lys	Pro	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
		355					360					365			
Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	Glu	Ser	Asn	Ile
	370					375					380				
Lys	Val	Leu	Pro	Thr	Trp	Ser	Thr	Pro	Val	His	Ala	Asp	Pro	Lys	Leu
385					390					395					400
Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr
			405						410					415	
Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Glu	Pro	Pro	Ala
		420						425					430		
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
	435						440					445			
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu
	450					455					460				
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
465					470					475					480
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
			485						490					495	
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
		500						505					510		
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
		515					520					525			
Leu	Pro	Pro	Arg												
			530												

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGGGTGA CCGTGCCCTC CAGCAGCTTG GGC

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGGGATC CGTCGTCCAG AGCCCGTCCA GCTCCCCGTC CTGGGCCTCA

50

(2) INFORMATION FOR SEQ ID NO:9:

(A) LENGTH: 33 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

33

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

33

(A) LENGTH: 15 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

15

(A) LENGTH: 42 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

48

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

36

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	33 bases
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

(A) LENGTH: 32 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

32

(A) LENGTH: 31 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

31

(A) LENGTH: 31 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: nucleic acid**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGTTGGTTT CTCAGGTTG TGTCTTCTG A

31

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Glu	His	Ser	Thr	Phe	Leu	Ser	Gly	Leu	Val	Leu	Ala	Thr	Leu	Leu		
				5					10					15			
Ser	Gln	Val	Ser	Pro	Phe	Lys	Ile	Pro	Ile	Glu	Glu	Leu	Glu	Asp	Arg		
			20					25					30				
Val	Phe	Val	Asn	Cys	Asn	Thr	Ser	Ile	Thr	Trp	Val	Glu	Gly	Thr	Val		
			35				40					45					
Gly	Thr	Leu	Leu	Ser	Asp	Ile	Thr	Arg	Leu	Asp	Leu	Gly	Lys	Arg	Ile		
			50			55				60							
Leu	Asp	Pro	Arg	Gly	Ile	Tyr	Arg	Cys	Asn	Gly	Thr	Asp	Ile	Tyr	Lys		
					70				75					80			
Asp	Lys	Glu	Ser	Thr	Val	Gln	Val	His	Tyr	Arg	Met	Cys	Gln	Ser	Cys		
				85				90					95				
Val	Glu	Leu	Asp	Pro	Ala	Thr	Val	Ala	Gly	Ile	Ile	Val	Thr	Asp	Val		
				100				105					110				
Ala	Ile	Thr	Leu	Leu	Leu	Ala	Leu	Gly	Val	Phe	Cys	Phe	Ala	Gly	His		
				115			120					125					
Glu	Thr	Gly	Arg	Leu	Ser	Gly	Ala	Ala	Asp	Thr	Gln	Ala	Leu	Leu	Arg		
				130			135				140						
Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr		
					150				155					160			
Ser	His	Leu	Gly	Gly	Asn	Trp	Ala	Arg	Asn	Lys							
				165					170								

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Glu	Gln	Gly	Lys	Gly	Leu	Ala	Val	Leu	Ile	Leu	Ala	Ile	Ile	Leu		
				5					10					15			
Leu	Gln	Gly	Thr	Leu	Ala	Gln	Ser	Ile	Lys	Gly	Asn	His	Leu	Val	Lys		
			20					25					30				
Val	Tyr	Asp	Tyr	Gln	Glu	Asp	Gly	Ser	Val	Leu	Leu	Thr	Cys	Asp	Ala		
			35				40					45					
Glu	Ala	Lys	Asn	Ile	Thr	Trp	Phe	Lys	Asp	Gly	Lys	Met	Ile	Gly	Phe		
			50			55					60						

Leu	Thr	Glu	Asp	Lys	Lys	Lys	Trp	Asn	Leu	Gly	Ser	Asn	Ala	Lys	Asp
65					70					75					80
Pro	Arg	Gly	Met	Tyr	Gln	Cys	Lys	Gly	Ser	Gln	Asn	Lys	Ser	Lys	Pro
				85					90					95	
Leu	Gln	Val	Tyr	Arg	Met	Cys	Gln	Asn	Cys	Ile	Glu	Leu	Asn	Ala	
			100				105						110		
Ala	Thr	Ile	Ser	Gly	Phe	Leu	Phe	Ala	Glu	Ile	Val	Ser	Ile	Phe	Val
		115				120						125			
Leu	Ala	Val	Gly	Val	Tyr	Phe	Ile	Ala	Gly	Gln	Asp	Gly	Val	Arg	Gln
	130					135					140				
Ser	Arg	Ala	Ser	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr
145					150					155					160
Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly
			165						170					175	
Asn	Gln	Leu	Arg	Arg	Asn										
			180												

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Pro	Gly	Gly	Leu	Glu	Ala	Leu	Arg	Ala	Leu	Pro	Leu	Leu	Leu	Phe
				5					10					15	
Leu	Ser	Tyr	Ala	Cys	Leu	Gly	Pro	Gly	Cys	Gln	Ala	Leu	Arg	Val	Glu
			20					25					30		
Gly	Gly	Pro	Pro	Ser	Leu	Thr	Val	Asn	Leu	Gly	Glu	Glu	Ala	Arg	Leu
		35					40					45			
Thr	Cys	Glu	Asn	Asn	Gly	Arg	Asn	Pro	Asn	Ile	Thr	Trp	Trp	Phe	Ser
		50				55					60				
Leu	Gln	Ser	Asn	Ile	Thr	Trp	Pro	Pro	Val	Pro	Leu	Gly	Pro	Gly	Gln
65					70					75					80
Gly	Thr	Thr	Gly	Gln	Leu	Phe	Phe	Pro	Glu	Val	Asn	Lys	Asn	Thr	Gly
			85						90					95	
Ala	Cys	Thr	Gly	Cys	Gln	Val	Ile	Glu	Asn	Asn	Ile	Leu	Lys	Arg	Ser
			100					105					110		
Cys	Gly	Thr	Tyr	Leu	Arg	Val	Arg	Asn	Pro	Val	Pro	Arg	Pro	Phe	Leu
		115					120					125			
Asp	Met	Gly	Glu	Gly	Thr	Lys	Asn	Arg	Ile	Ile	Thr	Ala	Glu	Gly	Ile
		130				135					140				
Ile	Leu	Leu	Phe	Cys	Ala	Val	Val	Pro	Gly	Thr	Leu	Leu	Leu	Phe	Arg
145					150					155					160
Lys	Arg	Trp	Gln	Asn	Glu	Lys	Phe	Gly	Val	Asp	Met	Pro	Asp	Asp	Tyr
			165						170					175	
Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Gly	Leu	Asn	Leu	Asp	Asp	Cys	Ser	Met
			180					185					190		
Tyr	Glu	Asp	Ile	Ser	Arg	Gly	Leu	Gln	Gly	Thr	Tyr	Gln	Asp	Val	Gly
		195					200					205			
Asn	Leu	His	Ile	Gly	Asp	Ala	Gln	Leu	Glu	Lys	Pro				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:27:

(A) LENGTH: 228 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

[illegible]